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# **Cerebrospinal fluid cell-free tumour DNA as a liquid biopsy for primary brain tumours and central nervous system metastases**

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**Running Title: ctDNA-based liquid biopsy in brain malignancies**

## **ABSTRACT**

Challenges in obtaining tissue specimens from patients with brain tumours limits diagnosis and molecular characterisation and impairs the development of better therapeutic approaches. The analysis of cell-free tumour DNA in plasma (considered a liquid biopsy) has facilitated the characterisation of extra-cranial tumours. However, cell-free tumour DNA in plasma is limited in quantity and may not reliably capture the landscape of genomic alterations of brain tumours. Here, we review recent work assessing the relevance of cell-free tumour DNA from cerebrospinal fluid in the characterisation of brain cancer. We focus on the advances in the use of the cerebrospinal fluid as a source of cell-free tumour DNA to facilitate diagnosis, reveal actionable genomic alterations, monitor responses to therapy, and capture tumour heterogeneity in patients with primary brain tumours and brain and leptomeningeal metastases. Profiling cerebrospinal fluid cell-free tumour DNA provides the opportunity to precisely acquire and monitor genomic information in real time and guide precision therapies.

**Keywords:** Cerebrospinal fluid, circulating cell-free tumour DNA, genomic characterisation, glioblastoma, brain metastasis, liquid biopsy, brain cancer.

## **KEY MESSAGE**

Challenges in systematically obtaining tumour tissue from brain primary tumours and metastases preclude their molecular characterisation and monitoring over time. Profiling cerebrospinal fluid cell-free tumour DNA provides an opportunity for precisely acquiring genomic information with the potential to facilitate diagnosis and precision therapies.

## Introduction

Genomic characterisation of tumour tissue has been established as crucial for state-of-the-art diagnostic and therapeutic approaches to cancer. However, characterisation of cancer is challenged by constitutive and evolving intra-tumour and inter-lesion heterogeneity which requires thorough and continuous analysis of genomic complexity over time. This is particularly relevant in brain malignancies where the genomic landscape changes in response to treatment or during relapse, and can differ from the primary extra-cranial lesion in the case of brain metastases. Yet, obtaining samples for characterisation and correct diagnosis can be difficult in brain cancer patients. The anatomical location of the tumour limits access due to the risk and complexity of intracranial surgical procedures.

Invasive surgical procedures have been the cornerstone treatment and a diagnostic tool in patients with primary brain tumours and in selected patients with brain metastasis. However, collecting tumour tissue from central nervous system (CNS) malignancies is complex, can be risky, and sometimes unfeasible, at least with purely diagnostic intent. Surgery has a role in improving disease control in patients with primary tumours or with a single, resectable brain metastasis, whereas patients with disseminated systemic disease are frequently not candidates for routine neurosurgical procedures [1, 2]. Moreover, specimens may be small and not representative hampering correct diagnosis or even necessitating multiple surgical samplings to clarify final pathological diagnosis. In addition, the surgical intervention strategy and assessment of the surgical risk-benefit balance depend on the tumour prognosis. This implies that an intraoperative histologic diagnosis may be required possibly delaying the surgical procedure. Repeat surgical interventions may be needed to differentiate tumour pseudoprogression induced by treatment from true relapse. The challenges in obtaining tumour tissue have led physicians to rely on primary archival tumour specimens. Thus, in some cases, therapies for brain cancer are selected based on the molecular characteristics of the primary tumour which can differ from the current tumour manifestation [3, 4].

Plasma cell-free circulating tumour DNA (ctDNA) has been used as a “liquid biopsy” in the context of tumour genomic characterisation [5-12]. ctDNA is the fraction of the total cell-free DNA that is derived from tumour cells and can be defined by the presence of genomic alterations. ctDNA detected in plasma has shown promise in characterising tumours and allowing patients and their cancers to be monitored over time. Analyses of mutations in plasma ctDNA have demonstrated high concordance with genomic alterations in the tumour [10].

However, in the context of primary brain tumours and brain metastasis, plasma ctDNA has been shown to be in low abundance and present in a limited number of patients [8, 13-16]. Importantly, the cerebrospinal fluid (CSF) is in intimate contact with brain malignancies and has been recently proven to contain ctDNA. The CSF space involves the intracerebral ventricles, subarachnoid spaces of the spine and brain (cisterns and sulci), and the central spinal cord canal. The CSF is renewed 3-5 times daily and is produced by the choroid plexus. The CSF circulates in a craniocaudal direction from ventricles to spinal subarachnoid space from where it is removed via craniocaudal lymphatic routes and the venous system[17]. The CSF space is separated from the vascular system by the blood-CSF barrier, while the blood-brain barrier is located between the brain parenchyma and the vascular system[18].

CSF has been explored as a source of ctDNA for precisely characterising brain cancers. Studies reported prior to the era of high-throughput sequencing showed that some molecular alterations or gene mutations can be detected in the DNA present in the CSF of patients with brain tumours [19-24]. Importantly, massively parallel sequencing methods have recently been used to analyse cell-free tumour DNA from CSF to comprehensively characterise somatic alterations including gene mutations and copy number alterations [15, 25-29] **(Table 1)**.

DNA was isolated from CSF (ranging from 0.75 - 10 ml) usually obtained from a lumbar puncture and DNA sequencing (i.e. droplet digital PCR, targeted sequencing, whole exome sequencing, or shallow whole genome sequencing) allowed the identification of ctDNA. Notably, CSF ctDNA enabled identification of genomic alterations in patients with systemic metastatic burden including brain metastasis, or disease restricted to the brain (primary tumours and brain metastasis) [15, 25-27]. Higher grade brain tumours were more likely to exhibit detectable CSF ctDNA than lower grade ones [26] and, in some cases, the distance of the tumour to CSF spaces could determine the amount of CSF ctDNA[27].

Here, we focus on the studies related to ctDNA obtained from CSF. Nowadays, the CSF liquid biopsy is increasingly allowing molecular diagnoses, providing information on prognosis, facilitating the identification of new actionable genomic alterations, aiding in monitoring response to therapy, and allowing deconvolution of tumour heterogeneity in patients with CNS cancer **(Figure 1)**.

## **Primary brain tumours**

### *Diagnostic considerations*

Primary brain tumours encompass a large variety of lesions with diverse natural course, response to treatment, and prognosis. The histological grade and molecular genetic make-up determine prognosis, with median overall survivals ranging from less than 1 year (e.g. in glioblastoma of the elderly) to long-term survival including cures (e.g. pilocytic astrocytoma and other rare circumscribed lesions). The clinical hallmark of glioblastoma is aggressive growth, local invasiveness and inexorable recurrence [30-32]. In recent years, the development of novel sequencing technologies and DNA methylation profiling coupled to bioinformatics tools has yielded an unparalleled, comprehensive view of the genome and epigenome of brain tumours [33-36].

The 2016 update of the WHO classification incorporated well established molecular parameters into the classification of brain tumours, specifically gliomas. The analysis of the CSF ctDNA of a cohort of diffuse gliomas indicated that they could be subtyped by analysing the IDH1 and IDH2, ATRX, TP53, TERT, H3F3A and HIST1H3B mutational status, facilitating the classification of diffuse gliomas and providing prognostic information [28]. Moreover, the presence of mutations in the TERT promoter found in CSF ctDNA correlated with outcome [37]. In the case of diffuse midline gliomas, the detection of *H3F3A* and *HIST1H3B* mutations in the CSF could confirm diagnosis [28]. This is of major relevance since the anatomical location of this type of tumours increases the risk of obtaining surgical specimens.

CSF ctDNA was detected in a large proportion of patients with brain primary tumours (Table 1). However, CSF ctDNA is not found in all brain tumours. For example, in some low grade gliomas, CSF ctDNA was not detected or was not informative [28]. Technological advances may improve sequencing sensitivity in the future, thus reducing the number of non-informative cases.

#### *Therapeutic considerations*

ctDNA diagnostic applications with potential therapeutic implications remain limited for adult patients with primary brain tumours. The most relevant biomarker for glioblastoma in terms of choice of therapy remains promoter methylation of the MGMT gene [38]. Efforts at the detection of *MGMT* promoter methylation in CSF of glioma patients showed higher sensitivity than in plasma [39]. Future applications with therapeutic impact are likely to include the monitoring of EGFRvIII and amplified EGFR in patients undergoing EGFR targeted therapy [40]. The evaluation of ctDNA during the follow-up of patients and especially at recurrence can confirm the molecular status and may help to deliver precision therapies.

#### **Brain metastases**

### *Diagnostic considerations*

Brain metastases from solid tumours are more frequent than primary brain tumours. They may occur in 20-40% of advanced stage cancers, particularly in lung cancer, breast cancer and melanoma [41-43]. Recent reports on the branched evolution of cancer at different sites including metastasis to the brain have reinforced the need of sequential molecular profiling across the disease trajectory [4, 44]. Brain metastases exhibit different genomic alterations than the primary extra-cranial tumours [4] indicating that the brain lesion-specific genomic alterations should be identified to select the optimal therapeutic approach [4, 45]. CSF ctDNA and not plasma ctDNA can be a good surrogate marker in such situations since ctDNA from brain lesions is enriched in the CSF.

Trunk mutations, present in all cancer cells, as well as private genomic alterations, present in just a subpopulation of cells or in specific metastatic lesions, can be identified in the CSF [15, 27]. This allows opportunities for deconvolving tumour heterogeneity. CSF and plasma ctDNA were compared in a series of samples that included multiregional metastatic sites from postmortem specimens of patients with disseminated breast cancers including brain metastases [15]. For example, mutations found in the CSF ctDNA allowed to discern the origin of leptomeningeal and brain metastasis implants separately in a patient with Li Fraumeni syndrome and two concurrent tumours, a metastatic breast cancer and esthesioneuroblastoma [15]. CSF ctDNA analysis captured trunk mutations and, importantly, private mutations to the brain and to the meningeal deposits. These observations highlight the potential applications of CSF ctDNA to complement diagnosis of brain metastasis.

### *Therapeutic considerations*

Several targeted therapeutic agents have demonstrated clinical activity against established brain metastases [46-55] and monitoring actionable mutations and therapy resistance using CSF ctDNA appears to be an application of CSF-based liquid biopsies that could be close to clinical practice.

First (erlotinib and gefitinib) and second-generation (afatinib) epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKI) have shown activity against brain metastasis from non-small cell lung cancers (NSCLC) that harbour *EGFR* mutations [56-58]. A number of third-generation EGFR TKI that also target mutant EGFR T790M, which confers therapeutic resistance, are in various phases of clinical investigation to target brain metastases (osimertinib, rociletinib, ASP-8273, HM-61713). In anaplastic lymphoma kinase gene (ALK)-rearranged (ALK)-NSCLC, second-generation ALK inhibitors with increased

potency such as alectinib and ceritinib have apparently superior CNS penetration compared with crizotinib and share significant therapeutic potential [53-55]. Breast cancer studies have focused primarily on targeted therapies (e.g., lapatinib, pertuzumab, ado-trastuzumab emtansine (T-DM1)) used for HER2-positive cancers [51, 52, 59, 60]. In patients with melanoma and brain metastases, substantial clinical activity has been observed with BRAF and MEK inhibitors, e.g., dabrafenib plus trametinib [49, 61], resulting in an intracranial response rate of nearly 60% [61]. Ongoing clinical trials exploit the cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4) and programmed death 1 (PD-1) pathways as target for immune checkpoint inhibitor therapy [50, 62]. Actionable genomic alterations with potential therapeutic implications have been identified in the CSF ctDNA [15, 25-27], including EGFR, ALK, HER2, BRAF-targetable kinases and others associated with DNA integrity such as *BRCA1* and *BRCA2* [63].

Analysis of CSF ctDNA has also shown gene mutations associated with therapy resistance [15, 27, 64]. Drug-resistance mutations in patients whose CNS disease progressed during TKI therapy (EGFR, ALK, HER2, or BRAF) were identified in CSF ctDNA in one-third of cases [27]. This included a *NRAS* G12R mutation in the CSF of a BRAF V600E-mutant (and *NRAS*-negative) melanoma; a *PIK3CA* H1047R mutation in the CSF of a HER2-amplified breast cancer patient, potentially associated with trastuzumab resistance; and an *EGFR* T790M mutation in the CSF of a patient with *EGFR*-mutant NSCLC who did not respond to a second-generation EGFR TKI [27]. *ESR1* mutations can confer resistance to aromatase inhibitor therapy in advanced estrogen receptor (ER)-positive breast cancers, but not to fulvestrant [65, 66]. A clinical trial is evaluating *ESR1* mutations in plasma ctDNA to predict the efficacy of a change of the hormone therapy (aromatase inhibitor changed to fulvestrant) (ClinicalTrials.gov Identifier: NCT03079011). Translation of this type of clinical trial design to the setting of patients with brain metastasis is envisioned using liquid biopsies. In the context of multiple metastases and discordant clinico-radiological findings, analysing a single-lesion biopsy is inadequate in guiding the selection of targeted therapy [67]. Parallel analyses of serial CSF and plasma ctDNA samples may be warranted.

Although the most common initial clinical presentation of metastatic HER2-positive breast cancer is with extra-cranial metastases, CNS progression occurs in a substantial proportion of patients during the course of the disease [68]. It has also been shown that extensive extra-CNS disease control, with HER2 targeting, might drive high incidence of CNS progression [69, 70]. This situation remains a major challenge where genomic analysis of ctDNA in the CSF might allow interrogation of the molecular status of progressive CNS metastasis. For example, in a case vignette, CSF ctDNA analysis captured CNS genomic alterations in patients with absent or minimal extracranial tumour disease burden, where



plasma ctDNA profiling did not play a diagnostic role [15]. A HER2-positive metastatic breast cancer patient with divergent responses of brain metastases underwent autopsy. Copy number alteration testing of three spatially separated brain metastases, in addition to CSF ctDNA and plasma ctDNA sampling, showed *ERBB2* amplification, a hallmark of HER2-positive breast cancer in CSF ctDNA and not in the plasma analysis [15].

## **Leptomeningeal metastases**

### *Diagnostic considerations*

Leptomeningeal metastasis, defined by the multifocal seeding of the leptomeninges by malignant cells, is a rare but often rapidly fatal manifestation of advanced cancer [71-73]. Diagnosing leptomeningeal metastasis relies on clinical symptomatology, MRI, and on detecting malignant cells in the CSF through CSF cytology. Its incidence is increasing and prognosis remains poor despite radiotherapy, systemic and intrathecal chemotherapy, and precision treatments in molecularly selected patients [71, 72].

Two principal diagnostic applications of ctDNA studies in patients with leptomeningeal metastasis emerge: first, detecting CSF ctDNA in patients with leptomeningeal metastasis may complement diagnostic profiling in patients with negative cytology, second, identifying actionable genomic alterations in CSF ctDNA has the potential to define an optimal targeted therapy[15]. CSF ctDNA revealed mutations in 50% of patients with primary brain tumours despite their CSF being negative for malignant cells [27], further, among patients with brain metastases, somatic mutations were found in 100% of patients with positive cytology and in 25% of patients with negative cytology [27].

A pivotal study compared CSF profiling with CSF cytology results in the same CSF extraction [15]. Analysis of three metastatic breast cancer patients with clinical signs and symptoms suggestive of leptomeningeal metastasis showed that CSF ctDNA analysis was more sensitive than cytology in detecting leptomeningeal metastasis, and leptomeningeal infiltration was confirmed during autopsy [15]. A molecular case report compared paired profiling of matched CSF ctDNA and plasma ctDNA from a patient with HER2-positive metastatic breast cancer. The patient developed CNS progression and leptomeningeal metastasis whereas the systemic extracranial metastases showed a clinical and radiological response to treatment with T-DM1 [74]. CSF ctDNA revealed an enrichment of *ERBB2* amplification, *MYC* amplification and *PIK3CA* and *TP53* driver gene mutations, presumably reflecting CNS

progression whereas decreasing mutant allelic fractions of selected mutations in plasma ctDNA likely reflected a partial clinical response in the extracranial compartment [74]. In metastatic melanoma spreading to the leptomeninges, CSF examination using PCR-based techniques has been successfully used for diagnosis and monitoring response to therapy based on the detection of driver mutations, e.g. affecting *BRAF*. [64, 75].

Further work is warranted to consolidate CSF ctDNA as a complementary tool for the diagnosis and characterization of leptomeningeal metastasis. Accordingly, the EANO ESMO guideline advises caution in over-interpreting ctDNA detected in CSF as a proof of leptomeningeal seeding.

### *Therapeutic considerations*

Recent and ongoing studies address the role of CSF ctDNA in patients with *EGFR*-mutant NSCLC and leptomeningeal metastasis [27, 64]. Forty NSCLC patients with suspected leptomeningeal metastasis were profiled, including 35 patients with a confirmed leptomeningeal metastases [64]. *EGFR* T790M and *MET* amplification were detected in 21% and 39% in CSF ctDNA, respectively, suggesting a resistance profile to *EGFR*-TKI associated with leptomeningeal disease. The BLOOM study (ClinicalTrials.gov Identifier: NCT02228369) investigates osimertinib, an oral, irreversible third-generation *EGFR* TKI selectively active against the *EGFR* T790M resistance mutation [76]. Encouraging activity has been seen in patients with leptomeningeal metastasis from NSCLC and results of *EGFR* mutant ctDNA analyses are being awaited (ClinicalTrials.gov Identifier: NCT02228369) [77]. Thus, ctDNA analysis should be considered for the *EGFR* and T790M status in the CSF at diagnosis and in case of suspicion of progression of NSCLC leptomeningeal metastases to guide the therapeutic decision.

### **Road to clinical practice**

To integrate the assessment of ctDNA obtained from CSF liquid biopsies into current standards of care, several questions and controversies have to be addressed. For almost all primary brain tumours, extent of resection is an important prognostic factor. Thus, situations where a surgical intervention is not an option, but a diagnosis would still be welcome, are rare. These might include patients with major comorbidities thought to be at high risk of complications, e.g., those with high bleeding risk for various reasons. Furthermore, there are instances where initial stereotactic biopsies of brain lesions are not informative and where non-neoplastic lesions, e.g., neuroinflammatory or neuroinfectious diseases are a differential diagnosis. In these cases, detection of tumour-defining genomic alterations in the CSF

ctDNA may greatly aid in further management. Furthermore, DNA methylation profiling may represent a novel approach that will undoubtedly also be explored for confirming tumour diagnoses from small tissue samples, including CSF [36]. Future studies will also need to determine in how far serial assessments of ctDNA load in the CSF may aid in situations where response assessment based on MRI alone remains challenging, including brain tumours treated with immunotherapy, and help clinical decision making.

The situation is different for patients with brain metastases from solid tumours. For brain metastases from unknown primary tumours, either rapid neurosurgical intervention as clinically needed or initial work-up by chest abdomen CT or FDG-PET are standard procedures [78] whereas liquid biopsies have so far not assumed a role. However, patients with new brain lesions detected by neuroimaging who are known to suffer from a malignancy are not routinely sent for neurosurgical resection unless this is thought to be in the best interest of the patient, e.g., because there are concerns regarding the validity of the radiological diagnosis, or because the patient is neurologically symptomatic. In such circumstances, notably with tumours with targetable lesions or in patients pre-exposed to chemotherapy or targeted therapy, it may be of major interest to ascertain whether the molecular tumour profile has changed, to select the most appropriate treatment. In such scenarios molecular tumour profiling from ctDNA from the CSF could become most valuable.

Similar considerations apply to patients with known leptomeningeal metastases, and targeted treatments are available for the major primary tumours associated with leptomeningeal metastasis: lung cancer, and breast cancer, and melanoma. The role of ctDNA in the CSF remains controversial if neither MRI nor routine CSF studies suggest the presence of leptomeningeal metastasis. In such situations, it can at present not be clarified whether ctDNA detected in the CSF signifies leptomeningeal tumour cell seeding. Thus, further studies are required to show that ctDNA in the CSF alone may justify treatment directed against leptomeningeal metastasis [79]. However the identification of the EGFR mutation or T790M in the CSF of patients with CNS metastases help guide the therapeutic decision in NSCLC patients.

Regarding the current data, ctDNA should be explored for the diagnosis and in case of suspicion of progression of leptomeningeal metastases. CSF and plasma ctDNA should be evaluated in parallel.

### **Current limitations**

Current data on ctDNA are mainly reported in small cohorts of patients, including sometimes different primary tumours. Analyses of large cohorts of patients should be performed. Technical issues such as the potential blood contamination in the CSF sample or the minimum time interval between surgery and CSF analysis for ctDNA have to be evaluated. Confirmation studies are needed to validate the role of ctDNA analysis for the diagnosis and follow-up of patients. Importantly, the feasibility of the CSF analysis in patients with brain tumours have to be considered when the lumbar puncture is contra-indicated due to risk of herniation related to the presentation of the space-occupying CNS tumours, or abnormal coagulation.

### **Conclusions and future perspectives**

Increasing understanding of the genomic and epigenomic characteristics of primary brain tumours and brain and leptomeningeal metastases has uncovered the extraordinary complexity of these tumours [4, 48, 80, 81]. Nevertheless, identifying biomarkers to assist in the diagnosis, prognosis, prediction of targeted therapy responses, serial monitoring and mechanisms of therapy resistance for patients with CNS malignancies [80] remains challenging, in part because of difficulties in accessing CNS tumour-derived tissue.

CNS malignancies demonstrate considerable spatial and temporal intratumour and inter-tumour heterogeneity. For patients with primary brain tumours or with brain metastases, identifying and monitoring brain-specific characteristics through CSF ctDNA may expedite the design of targeted therapies. Yet, no liquid circulating biomarkers have been validated and integrated into clinical practice for primary brain tumours or brain metastases. CSF ctDNA is a promising instrument to evaluate CNS malignancies in real-time and guide therapeutic management of patients.

The treatment of human cancer has shifted towards a precision medicine paradigm, in which the selection of a targeted therapy will rely upon the genetic anomalies in individual patients. We predict that characterising brain tumours will be feasible using CSF ctDNA in the near future. In addition, combining plasma ctDNA with CSF ctDNA, morphologic analyses and imaging methods would ideally be complementary for patients with brain metastases and systemic disseminated disease. Thus, liquid biopsy approaches based on CSF are opening new avenues for the better managing of brain cancer patients.

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## References

1. Owen S, Souhami L. The management of brain metastases in non-small cell lung cancer. *Front Oncol* 2014; 4: 248.
2. Ferguson SD, Wagner KM, Prabhu SS et al. Neurosurgical management of brain metastases. *Clin Exp Metastasis* 2017.
3. Johnson BE, Mazon T, Hong C et al. Mutational analysis reveals the origin and therapy-driven evolution of recurrent glioma. *Science* 2014; 343: 189-193.
4. Brastianos PK, Carter SL, Santagata S et al. Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. *Cancer Discov* 2015; 5: 1164-1177.
5. Best MG, Sol N, Ziji S et al. Liquid biopsies in patients with diffuse glioma. *Acta Neuropathol* 2015; 129: 849-865.
6. De Mattos-Arruda L, Cortes J, Santarpia L et al. Circulating tumour cells and cell-free DNA as tools for managing breast cancer. *Nat Rev Clin Oncol* 2013; 10: 377-389.
7. Murtaza M, Dawson SJ, Tsui DW et al. Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nature* 2013; 497: 108-112.
8. Bettegowda C, Sausen M, Leary RJ et al. Detection of circulating tumor DNA in early- and late-stage human malignancies. *Sci Transl Med* 2014; 6: 224ra224.
9. Siravegna G, Mussolin B, Buscarino M et al. Clonal evolution and resistance to EGFR blockade in the blood of colorectal cancer patients. *Nat Med* 2015; 21: 827.
10. Phallen J, Sausen M, Adleff V et al. Direct detection of early-stage cancers using circulating tumor DNA. *Sci Transl Med* 2017; 9.
11. Alix-Panabieres C, Pantel K. Clinical Applications of Circulating Tumor Cells and Circulating Tumor DNA as Liquid Biopsy. *Cancer Discov* 2016; 6: 479-491.
12. Siravegna G, Marsoni S, Siena S, Bardelli A. Integrating liquid biopsies into the management of cancer. *Nat Rev Clin Oncol* 2017; 14: 531-548.
13. Lavon I, Refael M, Zelikovitch B et al. Serum DNA can define tumor-specific genetic and epigenetic markers in gliomas of various grades. *Neuro Oncol* 2010; 12: 173-180.
14. Chen WW, Balaj L, Liao LM et al. BEAMing and Droplet Digital PCR Analysis of Mutant IDH1 mRNA in Glioma Patient Serum and Cerebrospinal Fluid Extracellular Vesicles. *Mol Ther Nucleic Acids* 2013; 2: e109.

15. De Mattos-Arruda L, Mayor R, Ng CK et al. Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma. *Nat Commun* 2015; 6: 8839.
16. Boisselier B, Gallego Perez-Larraya J, Rossetto M et al. Detection of IDH1 mutation in the plasma of patients with glioma. *Neurology* 2012; 79: 1693-1698.
17. Gherzi-Egea JF, Strazielle N, Catala M et al. Molecular anatomy and functions of the choroidal blood-cerebrospinal fluid barrier in health and disease. *Acta Neuropathol* 2018; 135: 337-361.
18. Redzic Z. Molecular biology of the blood-brain and the blood-cerebrospinal fluid barriers: similarities and differences. *Fluids Barriers CNS* 2011; 8: 3.
19. Schmitt-Graff A, Hummel M, Anagnostopoulos I et al. [Primary brain lymphoma in acquired immunodeficiency syndrome. Immunophenotype and molecular pathologic characterization in stereotactic biopsy, autopsy and cerebrospinal fluid cytology]. *Pathologe* 1995; 16: 75-80.
20. Rhodes CH, Honsinger C, Sorenson GD. PCR-detection of tumor-derived p53 DNA in cerebrospinal fluid. *Am J Clin Pathol* 1995; 103: 404-408.
21. Swinkels DW, de Kok JB, Hanselaar A et al. Early detection of leptomeningeal metastasis by PCR examination of tumor-derived K-ras DNA in cerebrospinal fluid. *Clin Chem* 2000; 46: 132-133.
22. Shi W, Lv C, Qi J et al. Prognostic value of free DNA quantification in serum and cerebrospinal fluid in glioma patients. *J Mol Neurosci* 2012; 46: 470-475.
23. Yang H, Cai L, Zhang Y et al. Sensitive detection of EGFR mutations in cerebrospinal fluid from lung adenocarcinoma patients with brain metastases. *J Mol Diagn* 2014; 16: 558-563.
24. Touat M, Duran-Pena A, Alentorn A et al. Emerging circulating biomarkers in glioblastoma: promises and challenges. *Expert Rev Mol Diagn* 2015; 15: 1311-1323.
25. Pan W, Gu W, Nagpal S et al. Brain tumor mutations detected in cerebral spinal fluid. *Clin Chem* 2015; 61: 514-522.
26. Wang Y, Springer S, Zhang M et al. Detection of tumor-derived DNA in cerebrospinal fluid of patients with primary tumors of the brain and spinal cord. *Proc Natl Acad Sci U S A* 2015; 112: 9704-9709.
27. Pentsova EI, Shah RH, Tang J et al. Evaluating Cancer of the Central Nervous System Through Next-Generation Sequencing of Cerebrospinal Fluid. *J Clin Oncol* 2016; 34: 2404-2415.

28. **Martinez-Ricarte F, Mayor R, Martinez-Saez E et al. Molecular Diagnosis of Diffuse Gliomas through Sequencing of Cell-Free Circulating Tumor DNA from Cerebrospinal Fluid. Clin Cancer Res 2018; 24: 2812-2819.**
29. **Mouliere F, Mair R, Chandrananda D et al. Detection of cell-free DNA fragmentation and copy number alterations in cerebrospinal fluid from glioma patients. EMBO Mol Med 2018.**
30. **Stupp R, Mason WP, van den Bent MJ et al. Radiotherapy plus concomitant and adjuvant temozolomide for glioblastoma. N Engl J Med 2005; 352: 987-996.**
31. **Furnari FB, Fenton T, Bachoo RM et al. Malignant astrocytic glioma: genetics, biology, and paths to treatment. Genes Dev 2007; 21: 2683-2710.**
32. **Omuro A, DeAngelis LM. Glioblastoma and other malignant gliomas: a clinical review. JAMA 2013; 310: 1842-1850.**
33. **Sottoriva A, Spiteri I, Piccirillo SG et al. Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. Proc Natl Acad Sci U S A 2013; 110: 4009-4014.**
34. **Cancer Genome Atlas Research N, Brat DJ, Verhaak RG et al. Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. N Engl J Med 2015; 372: 2481-2498.**
35. **Ceccarelli M, Barthel FP, Malta TM et al. Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell 2016; 164: 550-563.**
36. **Capper D, Jones DTW, Sill M et al. DNA methylation-based classification of central nervous system tumours. Nature 2018; 555: 469-474.**
37. **Juratli TA, Stasik S, Zolal A et al. TERT Promoter Mutation Detection in Cell-Free Tumor-Derived DNA in Patients with IDH Wild-Type Glioblastomas: A Pilot Prospective Study. Clin Cancer Res 2018; 24: 5282-5291.**
38. **Weller M, van den Bent M, Tonn JC et al. European Association for Neuro-Oncology (EANO) guideline on the diagnosis and treatment of adult astrocytic and oligodendroglial gliomas. Lancet Oncol 2017; 18: e315-e329.**
39. **Wang Z, Jiang W, Wang Y et al. MGMT promoter methylation in serum and cerebrospinal fluid as a tumor-specific biomarker of glioma. Biomed Rep 2015; 3: 543-548.**



40. Figueroa JM, Skog J, Akers J et al. Detection of wild-type EGFR amplification and EGFRvIII mutation in CSF-derived extracellular vesicles of glioblastoma patients. *Neuro Oncol* 2017; 19: 1494-1502.
41. Tabouret E, Chinot O, Metellus P et al. Recent trends in epidemiology of brain metastases: an overview. *Anticancer Res* 2012; 32: 4655-4662.
42. Taillibert S, Le Rhun E. [Epidemiology of brain metastases]. *Cancer Radiother* 2015; 19: 3-9.
43. Stelzer KJ. Epidemiology and prognosis of brain metastases. *Surg Neurol Int* 2013; 4: S192-202.
44. Paik PK, Shen R, Won H et al. Next-Generation Sequencing of Stage IV Squamous Cell Lung Cancers Reveals an Association of PI3K Aberrations and Evidence of Clonal Heterogeneity in Patients with Brain Metastases. *Cancer Discov* 2015; 5: 610-621.
45. Chen G, Chakravarti N, Aardalen K et al. Molecular profiling of patient-matched brain and extracranial melanoma metastases implicates the PI3K pathway as a therapeutic target. *Clin Cancer Res* 2014; 20: 5537-5546.
46. Rochet NM, Kottschade LA, Markovic SN. Vemurafenib for melanoma metastases to the brain. *N Engl J Med* 2011; 365: 2439-2441.
47. Welsh JW, Komaki R, Amini A et al. Phase II trial of erlotinib plus concurrent whole-brain radiation therapy for patients with brain metastases from non-small-cell lung cancer. *J Clin Oncol* 2013; 31: 895-902.
48. Seoane J, De Mattos-Arruda L. Brain metastasis: new opportunities to tackle therapeutic resistance. *Mol Oncol* 2014; 8: 1120-1131.
49. Long GV, Trefzer U, Davies MA et al. Dabrafenib in patients with Val600Glu or Val600Lys BRAF-mutant melanoma metastatic to the brain (BREAK-MB): a multicentre, open-label, phase 2 trial. *Lancet Oncol* 2012; 13: 1087-1095.
50. Margolin K, Ernstoff MS, Hamid O et al. Ipilimumab in patients with melanoma and brain metastases: an open-label, phase 2 trial. *Lancet Oncol* 2012; 13: 459-465.
51. Lin NU, Dieras V, Paul D et al. Multicenter phase II study of lapatinib in patients with brain metastases from HER2-positive breast cancer. *Clin Cancer Res* 2009; 15: 1452-1459.
52. Bachelot T, Romieu G, Campone M et al. Lapatinib plus capecitabine in patients with previously untreated brain metastases from HER2-positive metastatic breast cancer (LANDSCAPE): a single-group phase 2 study. *Lancet Oncol* 2013; 14: 64-71.

53. Gadgeel SM, Gandhi L, Riely GJ et al. Safety and activity of alectinib against systemic disease and brain metastases in patients with crizotinib-resistant ALK-rearranged non-small-cell lung cancer (AF-002JG): results from the dose-finding portion of a phase 1/2 study. *Lancet Oncol* 2014; 15: 1119-1128.
54. Costa DB, Shaw AT, Ou SH et al. Clinical Experience With Crizotinib in Patients With Advanced ALK-Rearranged Non-Small-Cell Lung Cancer and Brain Metastases. *J Clin Oncol* 2015; 33: 1881-1888.
55. Crino L, Ahn MJ, De Marinis F et al. Multicenter Phase II Study of Whole-Body and Intracranial Activity With Ceritinib in Patients With ALK-Rearranged Non-Small-Cell Lung Cancer Previously Treated With Chemotherapy and Crizotinib: Results From ASCEND-2. *J Clin Oncol* 2016.
56. Iuchi T, Shingyoji M, Sakaida T et al. Phase II trial of gefitinib alone without radiation therapy for Japanese patients with brain metastases from EGFR-mutant lung adenocarcinoma. *Lung Cancer* 2013; 82: 282-287.
57. Porta R, Sanchez-Torres JM, Paz-Ares L et al. Brain metastases from lung cancer responding to erlotinib: the importance of EGFR mutation. *Eur Respir J* 2011; 37: 624-631.
58. Schuler M, Wu YL, Hirsh V et al. First-Line Afatinib versus Chemotherapy in Patients with Non-Small Cell Lung Cancer and Common Epidermal Growth Factor Receptor Gene Mutations and Brain Metastases. *J Thorac Oncol* 2016; 11: 380-390.
59. Swain SM, Baselga J, Miles D et al. Incidence of central nervous system metastases in patients with HER2-positive metastatic breast cancer treated with pertuzumab, trastuzumab, and docetaxel: results from the randomized phase III study CLEOPATRA. *Ann Oncol* 2014; 25: 1116-1121.
60. Bartsch R, Berghoff AS, Preusser M. Breast cancer brain metastases responding to primary systemic therapy with T-DM1. *J Neurooncol* 2014; 116: 205-206.
61. Davies MA, Saiag P, Robert C et al. Dabrafenib plus trametinib in patients with BRAFV600-mutant melanoma brain metastases (COMBI-MB): a multicentre, multicohort, open-label, phase 2 trial. *Lancet Oncol* 2017; 18: 863-873.
62. Berghoff AS, Preusser M. Targeted Therapies for Melanoma Brain Metastases. *Curr Treat Options Neurol* 2017; 19: 13.
63. Chakravarty D, Gao J, Phillips S et al. OncoKB: A Precision Oncology Knowledge Base. *JCO Precision Oncology* 2017; 1-16.

64. Jiang B-Y, LI Y, Chuai S et al. NGS to reveal heterogeneity between cerebrospinal fluid and plasma ctDNA among non-small cell lung cancer patients with leptomeningeal carcinomatosis. *J Clin Oncol* 2017; 35: 9022.
65. Spoerke JM, Gendreau S, Walter K et al. Heterogeneity and clinical significance of ESR1 mutations in ER-positive metastatic breast cancer patients receiving fulvestrant. *Nat Commun* 2016; 7: 11579.
66. Fribbens C, O'Leary B, Kilburn L et al. Plasma ESR1 Mutations and the Treatment of Estrogen Receptor-Positive Advanced Breast Cancer. *J Clin Oncol* 2016; 34: 2961-2968.
67. Russo M, Siravegna G, Blaszkowsky LS et al. Tumor Heterogeneity and Lesion-Specific Response to Targeted Therapy in Colorectal Cancer. *Cancer Discov* 2016; 6: 147-153.
68. Bendell JC, Domchek SM, Burstein HJ et al. Central nervous system metastases in women who receive trastuzumab-based therapy for metastatic breast carcinoma. *Cancer* 2003; 97: 2972-2977.
69. Martin AM, Cagney DN, Catalano PJ, et al. Brain metastases in newly diagnosed breast cancer: A population-based study. *JAMA Oncology* 2017.
70. Friedigkeit N, Hartmaier RJ, Chen Y, et al. Intrinsic subtype switching and acquired erbb2/her2 amplifications and mutations in breast cancer brain metastases. *JAMA Oncology* 2016.
71. Remon J, Le Rhun E, Besse B. Leptomeningeal carcinomatosis in non-small cell lung cancer patients: A continuing challenge in the personalized treatment era. *Cancer Treat Rev* 2017; 53: 128-137.
72. Dudani S, Mazzarello S, Hilton J et al. Optimal Management of Leptomeningeal Carcinomatosis in Breast Cancer Patients-A Systematic Review. *Clin Breast Cancer* 2016; 16: 456-470.
73. Le Rhun E, Weller M, Brandsma D et al. EANO-ESMO Clinical Practice Guidelines for diagnosis, treatment and follow-up of patients with leptomeningeal metastasis from solid tumours. *Ann Oncol* 2017; 28: iv84-iv99.
74. Siravegna G, Geuna E, Mussolin B et al. Genotyping tumor DNA in cerebrospinal fluid and plasma in a HER2 positive breast cancer with brain metastases. *ESMO Open* 2017.
75. Taillibert S, Chamberlain MC. Leptomeningeal metastasis. *Handb Clin Neurol* 2018; 149: 169-204.

76. Ballard P, Yates JW, Yang Z et al. Preclinical Comparison of Osimertinib with Other EGFR-TKIs in EGFR-Mutant NSCLC Brain Metastases Models, and Early Evidence of Clinical Brain Metastases Activity. *Clin Cancer Res* 2016; 22: 5130-5140.
77. Yang JC-H, Cho BC, Kim D-W et al. Osimertinib for patients (pts) with leptomeningeal metastases (LM) from EGFR-mutant non-small cell lung cancer (NSCLC): Updated results from the BLOOM study. *J Clin Oncol* 2017; 35: 9022.
78. Wolpert F, Weller M, Berghoff AS et al. Diagnostic value of (18)F-fluorodesoxyglucose positron emission tomography for patients with brain metastasis from unknown primary site. *Eur J Cancer* 2018; 96: 64-72.
79. Le Rhun E, Bertrand N, Dumont A et al. Identification of single nucleotide polymorphisms of the PI3K-AKT-mTOR pathway as a risk factor of central nervous system metastasis in metastatic breast cancer. *Eur J Cancer* 2017; 87: 189-198.
80. Tanaka S, Louis DN, Curry WT et al. Diagnostic and therapeutic avenues for glioblastoma: no longer a dead end? *Nat Rev Clin Oncol* 2013; 10: 14-26.
81. Dagogo-Jack I, Gill CM, Cahill DP et al. Treatment of brain metastases in the modern genomic era. *Pharmacol Ther* 2017; 170: 64-72.

## Figure legend

**Figure 1.** Potential use of CSF ctDNA as a liquid biopsy for primary brain tumours and brain metastasis

Reviewer: 1

#### Comments to the Author

The manuscript by Seoane et al. reviews the recent research on the use of cerebrospinal fluid (CSF) cell-free circulating tumour DNA (ctDNA) as diagnostic biomarker for patients with primary and secondary brain tumors. The most important comment is that expert analysis could be significantly strengthened throughout the manuscript so that the reader gains true understanding of where this field is. Below are some suggestions the authors can consider to further improve their manuscript.

1) The review would benefit from a succinct paragraph or figure describing the ventricular system and CSF circulation, as well as brain-CSF interface/barrier. The assumption that CSF ctDNA assessment is superior to plasma ctDNA seems based on a small number of pilot studies (see Table). It is unclear whether higher yields of ctDNA seen with CSF are explained by unique physiological properties of this compartment or by the inclusion of patients with leptomeningeal disease. Moreover, it is unclear whether failure to assess plasma ctDNA in some studies is explained by the absence of plasma ctDNA in most patients or by limitations with currently available technologies (ie need of higher sequencing depth for assessing plasma ctDNA), as prior studies suggested the presence of circulating DNA even in patients with low-grade gliomas (see PMID 23035067).

We agree with the reviewer. We have now included a paragraph describing the CSF circulation as well as the brain-CSF barrier in the Introduction. We have also discussed the referee's points stressing the limitations of the pilot studies and the current available technologies. We have cited PMID 23035067 and we have included in Table 1 the precise diagnoses of the analyzed cases showing the results of patients with tumours other than leptomeningeal metastasis.

2) The review would benefit from a succinct paragraph or table summarizing the methodologies currently available, as well as the currently ongoing prospective studies evaluating CSF ctDNA in patients with primary and secondary brain tumors.

We thank the reviewer for raising this point. We have now included a fragment about methodologies in the text, and a column describing the methodologies used by the different studies in Table 1.

3) Data from patients with primary and secondary brain tumors is often presented together, which makes sometimes difficult to understand the potential of CSF ctDNA in each clinical situation. The review would likely benefit from slightly reorganizing the paragraphs to present separately the main messages from studies in primary vs secondary brain tumors. Moreover, data from patients with leptomeningeal disease should be presented separately as it is unclear whether findings in this population will be applicable to patients without leptomeningeal disease.

We apologize for the lack of clarity. We have rewritten the manuscript following the reviewer recommendations and have now three new sections: *Primary brain tumors*, *Brain metastases* and *Leptomeningeal metastases*. Each of the sections including two subsections: *Diagnostic considerations* and *Therapeutic considerations*.

4) The authors could discuss more thoroughly the strengths and limitations of the studies presented in their manuscript, especially when discussing pilot studies which need further validation. For instance, throughout the manuscript, the authors cite one of their studies (ref.

20) without discussing the potential limitations of this work. The limitations of CSF puncture (ie patient's refusal, contraindication) could also be mentioned.

We agree with the reviewer. We have now included a section entitled: *Current limitations*, where we stated the lack of analyses of large cohorts of patients and the limitations of lumbar puncture, among other things. We have also included a column in Table 1 stating the number of patients in each study.

5) In Table 1, it would be helpful to provide patient numbers for each study/disease group in the first column, and precise some diagnoses (eg "Primary brain and spinal cord tumours"). "CSF detection" should be replaced with "Method for CSF collection"

We followed the reviewer's comments and included the number of patients for each study, stated more precise diagnoses, and inserted a column for methods.

6) The Figure does not provide much information and some parts seem speculative given the currently available data (eg lack of robust data suggesting that CSF ctDNA will allow discerning pseudoprogression from true progression in patients with gliomas). Would suggest removing or changing the title.

We have changed the title of the figure by: "Potential use of CSF ctDNA as a liquid biopsy for primary brain tumours and brain metastasis". Moreover, we have deleted the concepts of *pseudoprogression* and *pseudoregression* from Fig.1.

Reviewer: 2

Comments to the Author

Seoane and colleagues did a quality review on liquid biopsy in neuro-oncology, particularly in the field of circulating tumor-derived cell free DNA in CSF.

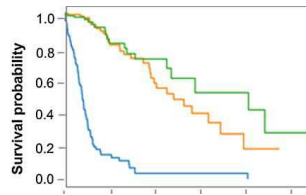
The authors have well presented the interest of CSF both in primary and secondary brain tumors. Two comments are suggested.

1/ The authors propose that CSF could be used for diagnosis, particularly in case of contraindication to surgery, and treatment follow-up. The collection of CSF is at risk of rare but severe complications (cerebral involvement with bulky tumors, spinal bleeding, etc.) that could occur in the population of patients suffering from brain tumors. The authors should discuss this point. If the information is available, it could be of interest to know the amount of CSF needed for ctDNA analyzes and to specify the sequencing techniques in presented studies (Table 1).

We thank the reviewer for raising this point. We have now included a section entitled: *Current limitations*, where we stated the limitations of lumbar puncture, among other things. We have also included a column in Table 1 stating the methodologies used in each study and inserted a paragraph in the Introduction describing the general methodology of CSF ctDNA analysis specifying the required CSF volume.

2/ Regarding the impact of CSF ctDNA on survival, the authors should discuss the recent results of Juratli et al (Clin Cancer Research, 2018).

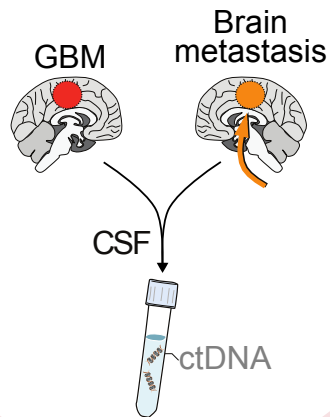
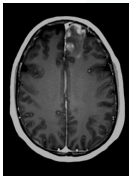
We thank the reviewer for noting this interesting article. We have now discussed the Juratli et al. work in the manuscript.



## Molecular diagnosis, prognosis

IDH1, IDH2, TP53, ATRX, TERT,  
H3F3A, HIST1H3B

Monitor tumour  
burden

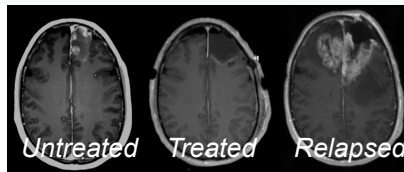


BRAF,  
EGFR,  
ALK, ...

Actionable  
genomic  
alterations

Primary vs metastasis  
Primary vs relapse

Evolving heterogeneity  
(tracking diversity and evolution)





Patient population	Sequencing technologies	Method for CSF collection / amount collected	Tumour-derived DNA found in CSF	Main findings	Comparison with plasma ctDNA	Extra-cranial disease analysed	Refs.
4 glioblastoma, 2 medulloblastoma, and 17 brain metastases (from breast and NSCLC)	Targeted capture massively parallel sequencing, digital droplet PCR	Lumbar puncture, cerebral shunts, autopsy /	58%	CSF ctDNA is enriched in brain tumours and produces better results than plasma ctDNA.	√	√	[15]
35 primary brain and spinal cord tumours	Targeted capture massively parallel sequencing, whole exome sequencing in four cases	Cerebral shunts (during surgical procedure)/ average of 4.8 mL (range = 0.75–10 mL).	74%	All adjacent tumours to the CSF reservoir had CSF ctDNA detectable.	--	--	[26]
12 primary brain tumours and 41 brain metastases	Targeted capture massively parallel sequencing	Lumbar puncture and 1 sample Ommaya reservoir / 5 ml of CSF	50-63%	Drug-resistance mutations in patients whose CNS disease progresses during kinase inhibitor therapy is identified in CSF ctDNA.	--	√	[27]
a vestibular schwannoma, a meningioma, 5 brain metastases and 3 leptomeningeal metastases	Targeted amplicon sequencing and digital PCR	Lumbar puncture, cerebral shunts (during surgical procedure) / 1–10 mL of CSF	85%	Tumour mutations were detectable in the CSF ctDNA of patients with different types of brain tumours.	√	--	[25]
20 primary diffuse glioma tumours	Targeted amplicon sequencing and digital PCR.	Lumbar puncture prior to surgery; 2 samples cisterna magna, 1 sample cerebral shunt / 2ml of CSF	85%	A sequencing platform to simultaneously test seven genes <i>IDH1</i> , <i>IDH2</i> , <i>TP53</i> , <i>ATRX</i> , <i>TERT</i> , <i>H3F3A</i> , <i>HIST1H3B</i> in the CSF ctDNA allowing the subclassification of diffuse glioma	--	--	[28]
38 TERT mutant glioblastoma (34 primary and 4 recurrent glioblastoma)	Sequenced uni-directionally on an Ion Torrent PGM NGS system, digital droplet PCR	Directly after opening the dura (durotomy), through dissection of the convexity subarachnoid space / 2-4 ml of CSF	92.1%	CSF ctDNA identifies <i>TERT</i> promoter mutations	√		[37]
13 glioma tumours	Untargeted, low-coverage WGS (< 0.4x) to detect SCNAs	Lumbar puncture / 10 ml of CSF	38.4%	Combining analyses of SCNAs with DNA fragmentation allows detection of ctDNA in CSF using sWGS data at low cost	--	--	[29]

Abbreviations: CNS, central nervous system; GBM, glioblastoma; LM, Leptomeningeal metastasis; NSCLC, non-small cell lung cancer; SCNAs, somatic copy number alterations; s-WGS, shallow whole-genome sequencing.